

EXHIBIT D:
COMPARISON OF RAT AND HUMAN LKB1

BLAST**Basic Local Alignment Search Tool**

[Edit and Resubmit](#) [Save Search Strategies](#) [Formatting options](#) [Download](#)

Blast 2 sequences

SEQ ID NO: 6

Results for: [|cl|17777 SEQ ID NO: 6\(433aa\)](#)

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

[|cl|17777](#)

[|cl|17777](#)

Description

SEQ ID NO: 6

Molecule type

amino acid

Query Length

433

Subject ID

[gi|157820995|ref|NP_001101539.1|](#)

Description

serine/threonine-protein kinase 11 [Rattus norvegicus] >[gi|149034596|gb|EDL89333.1|](#) serine/threonine kinase 11 (predicted), isoform CRA_a [Rattus norvegicus]

Molecule type

amino acid

Subject Length

436

Program

BLASTP 2.2.24+ [Citation](#)

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Reference - compositional score matrix adjustment

Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109.

Other reports: [Search Summary](#) [\[Taxonomy reports\]](#) [\[Multiple alignment\]](#)

[Search Parameters](#)

Search parameter name Search parameter value

Program	blastp
Query range	44-343
Word size	3
Expect value	10
Hitlist size	100
Gapcosts	11,1
Matrix	BLOSUM62

Low Complexity Filter	Yes
Filter string	L;
Genetic Code	1
Window Size	40
Threshold	11
Composition-based stats	2

Karlin-Altschul statistics

Params Ungapped Gapped

Lambda	0.320459	0.267
K	0.139595	0.041
H	0.429592	0.14

Results Statistics

Results Statistics parameter name Results Statistics parameter value

Effective search space	110297
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Graphic Summary**Distribution of Blast Hits on the Query Sequence****[?]**

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

[Dot Matrix View](#)**Plot of lcl|17777 vs gi|157820995|ref|NP_001101539.1| [?]**

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.

**Descriptions**

Sequences producing significant alignments:		Score (Bits)	E Value
ref NP_001101539.1	serine/threonine-protein kinase 11 [Rattu...	525	1e-153

Alignments

>ref|NP_001101539.1| serine/threonine-protein kinase 11 [Rattus norvegicus]
 gb|EDL89333.1| serine/threonine kinase 11 (predicted), isoform CRA_a [Rattus norvegicus]
 Length=436

Score = 525 bits (1351), Expect = 1e-153, Method: Compositional matrix adjust.
 Identities = 287/300 (96%), Positives = 291/300 (97%), Gaps = 0/300 (0%)

Query	44	KLIGKYLMDLLGEGSYGKVKEVLDSETLCRRAVKILKKKKLRRIPNGEANVKKEIQLLR	103
		KLIGKYLMDLLGEGSYGKVKEVLDSETLCRRAVKILKKKKLRRIPNGEANVKKEIQLLR	
Sbjct	44	KLIGKYLMDLLGEGSYGKVKEVLDSETLCRRAVKILKKKKLRRIPNGEANVKKEIQLLR	103
Query	104	RLRHKNVIQLVDVLYNEEKQKMYMVMMEYCVCGMQEMLDSVPEKRFPVCQAHGYFCQLIDG	163
		RLRH+NVQLVDVLYNEEKQKMYMVMMEYCVCGMQEMLDSVPEKRFPVCQAHGYF QLIDG	
Sbjct	104	RLRHRNVIQLVDVLYNEEKQKMYMVMMEYCVCGMQEMLDSVPEKRFPVCQAHGYFRQLIDG	163
Query	164	LEYLHSQGIVHKDIKPGNlllttggtlKISDLGVAEALHPFAADDTCRTSQGSPAFQPPE	223
		LEYLHSQGIVHKDIKPGNLLLT GTLKISDLGVAEALHPFA DDTCRTSQGSPAFQPPE	
Sbjct	164	LEYLHSQGIVHKDIKPGNLLLTNGTLKISDLGVAEALHPFAVDDTCRTSQGSPAFQPPE	223
Query	224	IANGLDTFSGFKVDIWSAGVTLYNITTGLYPFEGDNIYKLFENIGKGSYAIPGDCGPPLS	283
		IANGLDTFSGFKVDIWSAGVTLYNITTGLYPFEGDNIYKLFENIG+G + IP DC PPLS	
Sbjct	224	IANGLDTFSGFKVDIWSAGVTLYNITTGLYPFEGDNIYKLFENIGRGDFTIPDCAPPLS	283
Query	284	DLLKGMLEYEPAKRFSIRQIRQHSWFRKKHppaeapvpippspDTKDRWRSMTVVPYLED	343
		DLL+GMLEYEPAKRFSIRQIRQHSWFRKKHP AEA VPIPPSPDTKDRWRSMTVVPYLED	
Sbjct	284	DLLRGMLEYEPAKRFSIRQIRQHSWFRKKHPLAEALVPIPPSPDTKDRWRSMTVVPYLED	343